

SEQUENCE LISTING

<110> Lukyanov, Sergey
 Fradkov, Arcady
 Labas, Yulii
 Matz, Mikhail
 Lukyanov, Konstantin
 Gurskaya, Nadezda

<120> FAR RED SHIFTED FLUORESCENT PROTEINS

<130> CLON-028WO

<140> Unassigned

<141> 2001-10-12

<150> 60/240,018

<151> 2000-10-12

<150> 60,306,131

<151> 2001-07-16

<160> 28

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 910

<212> DNA

<213> heteractis crispa

<400> 1

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tacatggaag gcacgggttaa tggccattat ttcaagtgtg aaggagaggg agacggcaac 180
ccatttacag gtacgcagag catgaggatt catgtcaccg aaggggctcc attaccattt 240
gccttcgaca ttttggcacc gtgttgtagag tacggcagca ggacctttgt ccaccatacg 300
gcagagattc cagatttctt caagcagtct ttcctgaag gctttacttg ggaaagaacc 360
acaacctatg aagatggagg cattcttact gctcatcagg acacaagcct ggaggggaac 420
tgctttatat acaaggtgaa agtccttggt accaattttc ctgctgatgg ccccgatgatg 480
aagaacaaat caggaggatg ggagccatgc actgaggtgg tttatccaga gaatggtgtc 540
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tatacttctt acaggtccaa gaaagcagtc cgtgccttga caatgccagg atttcatttt 660
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gcactctgtg ctaggtacag tgatcttctt gaaaaagcaa attgattgtt cccagtgaca 780
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<210> 2

<211> 227

<212> PRT

<213> heteractis crispa

<400> 2

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      20           25           30
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Asn Pro Phe Thr Gly Thr Gln Ser Met Arg Ile His Val Thr Glu Gly
 35 40 45
 Ala Pro Leu Pro Phe Ala Phe Asp Ile Leu Ala Pro Cys Cys Glu Tyr
 50 55 60
 Gly Ser Arg Thr Phe Val His His Thr Ala Glu Ile Pro Asp Phe Phe
 65 70 75 80
 Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr
 85 90 95
 Glu Asp Gly Gly Ile Leu Thr Ala His Gln Asp Thr Ser Leu Glu Gly
 100 105 110
 Asn Cys Leu Ile Tyr Lys Val Lys Val Leu Gly Thr Asn Phe Pro Ala
 115 120 125
 Asp Gly Pro Val Met Lys Asn Lys Ser Gly Gly Trp Glu Pro Cys Thr
 130 135 140
 Glu Val Val Tyr Pro Glu Asn Gly Val Leu Cys Gly Arg Asn Val Met
 145 150 155 160
 Ala Leu Lys Val Gly Asp Arg Arg Leu Ile Cys His Leu Tyr Thr Ser
 165 170 175
 Tyr Arg Ser Lys Lys Ala Val Arg Ala Leu Thr Met Pro Gly Phe His
 180 185 190
 Phe Thr Asp Ile Arg Leu Gln Met Pro Arg Lys Thr Lys Asp Glu Tyr
 195 200 205
 Phe Glu Leu Tyr Glu Ala Ser Val Ala Arg Tyr Ser Asp Leu Pro Glu
 210 215 220
 Lys Ala Asn
 225

<210> 3
 <211> 908
 <212> DNA
 <213> heteractis crispa

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 ggaaggcagc gttaatggcc attatttcaa gtgtgaagga gagggagacg gcaaccatt 180
 tacaggtacg cagagcatga ggattcatgt caccgaagg gctccattac catttgctt 240
 cgacattttg gcaccgtgtt gtgagtagcg cagcaggacc tttgtccacc atacggcaga 300
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 ctatgaagat ggaggcattc ttactgctca tcaggacaca agcctggagg ggaactgcct 420
 tatatacaag gtgaaagtcc ttggtaccaa tttcctgct gatggccccg tgatgaagaa 480
 caaatcagaa ggatgggagc catgcactga ggtggtttat ccagataatg gtgtcctgtg 540
 tggacgtaat gtgatggccc ttaaagtcgg tgatcgtcgt ttgatctgcc atctctatac 600
 ttcttacagg tccaagaaag cagtcctgtc cttgacaatg ccaggatttc attttacaga 660
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 tgtggctagg tacagtgatc ttctgaaaa agcaaattga ttgttcccag tgacaccaga 780
 ctgctgtcag cttttggtta aagcccgaag gacaaaagga catttgtagt tttagtttat 840
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 ttaaacct 908

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 <211> 227
 <212> PRT
 <213> heteractis crispa

<400> 4
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 20 25 30

Asn Pro Phe Thr Gly Thr Gln Ser Met Arg Ile His Val Thr Glu Gly
 35 40 45
 Ala Pro Leu Pro Phe Ala Phe Asp Ile Leu Ala Pro Cys Cys Glu Tyr
 50 55 60
 Gly Ser Arg Thr Phe Val His His Thr Ala Glu Ile Pro Asp Phe Phe
 65 70 75 80
 Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr
 85 90 95
 Glu Asp Gly Gly Ile Leu Thr Ala His Gln Asp Thr Ser Leu Glu Gly
 100 105 110
 Asn Cys Leu Ile Tyr Lys Val Lys Val Leu Gly Thr Asn Phe Pro Ala
 115 120 125
 Asp Gly Pro Val Met Lys Asn Lys Ser Glu Gly Trp Glu Pro Cys Thr
 130 135 140
 Glu Val Val Tyr Pro Asp Asn Gly Val Leu Cys Gly Arg Asn Val Met
 145 150 155 160
 Ala Leu Lys Val Gly Asp Arg Arg Leu Ile Cys His Leu Tyr Thr Ser
 165 170 175
 Tyr Arg Ser Lys Lys Ala Val Arg Ala Leu Thr Met Pro Gly Phe His
 180 185 190
 Phe Thr Asp Ile Arg Leu Gln Met Pro Arg Lys Thr Lys Asp Glu Tyr
 195 200 205
 Phe Glu Leu Tyr Glu Ala Ser Val Ala Arg Tyr Ser Asp Leu Pro Glu
 210 215 220
 Lys Ala Asn
 225

<210> 5
 <211> 684
 <212> DNA
 <213> heteractis crispa

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 atgaggattc atgtcaccga aggggctcca ttaccatttg ccttcgacat tttggcaccg 180
 tgttgtgagt acggcagcag gacctttgtc caccatacgg cagagattcc cgatttcttc 240
 aagcagtctt tccctgaagg ctttacttgg gaaagaacca caacctatga agatggaggc 300
 attcttactg ctcatcagga cacaagcctg gaggggaact gccttatata caagtgaaa 360
 gtccttggtg ccaattttcc tgctgatggc cccgtgatga agaacaaatc aggaggatgg 420
 gagccaagca ctgaggtggt ttatccagag aatggtgtcc tgtgtggacg taatgtgatg 480
 gcccttaaag tcggtgatcg tcgtttgatc tgccatctct atacttctta caggtccaag 540
 aaagcagtcc gtgccttgac aatgccagga tttcatttta cagacatccg ccttcagatg 600
 ccgaggaaaa cgaaagacga gtactttgaa ctgtacgaag catctgtggc taggtacagt 660
 gatcttcctg aaaaagcaaa ttga 684

<210> 6
 <211> 227
 <212> PRT
 <213> heteractis crispa

<400> 6
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 Gly Thr Val Asn Gly His Tyr Phe Lys Cys Glu Gly Glu Gly Asp Gly
 20 25 30
 Asn Pro Phe Thr Gly Thr Gln Ser Met Arg Ile His Val Thr Glu Gly
 35 40 45
 Ala Pro Leu Pro Phe Ala Phe Asp Ile Leu Ala Pro Cys Cys Glu Tyr
 50 55 60

Gly Ser Arg Thr Phe Val His His Thr Ala Glu Ile Pro Asp Phe Phe
 65 70 75 80
 Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr
 85 90 95
 Glu Asp Gly Gly Ile Leu Thr Ala His Gln Asp Thr Ser Leu Glu Gly
 100 105 110
 Asn Cys Leu Ile Tyr Lys Val Lys Val Leu Gly Thr Asn Phe Pro Ala
 115 120 125
 Asp Gly Pro Val Met Lys Asn Lys Ser Gly Gly Trp Glu Pro Ser Thr
 130 135 140
 Glu Val Val Tyr Pro Glu Asn Gly Val Leu Cys Gly Arg Asn Val Met
 145 150 155 160
 Ala Leu Lys Val Gly Asp Arg Arg Leu Ile Cys His Leu Tyr Thr Ser
 165 170 175
 Tyr Arg Ser Lys Lys Ala Val Arg Ala Leu Thr Met Pro Gly Phe His
 180 185 190
 Phe Thr Asp Ile Arg Leu Gln Met Pro Arg Lys Thr Lys Asp Glu Tyr
 195 200 205
 Phe Glu Leu Tyr Glu Ala Ser Val Ala Arg Tyr Ser Asp Leu Pro Glu
 210 215 220
 Lys Ala Asn
 225

<210> 7
 <211> 681
 <212> DNA
 <213> heteractis crispa

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 aggattcatg tcaccgaagg ggctccatta ccatttgcct tcgacatttt ggcaccgtgt 180
 tgtgagtacg gcagcaggac ctttgtccac catacggcag agattcccga tttcttcaag 240
 cagtctttcc ctgaaggctt tacttgggaa agaaccacaa cctatgaaga tggaggcatt 300
 cttactgctc atcaggacac aagcctggag gggaaactgcc ttatatacaa ggtgaaagtc 360
 cttggtacca attttcctgc tgatggcccc gtgatgaaga acaaatcagg aggatgggag 420
 ccaagcactg aggtgggttta tccagagaat ggtgtcctgt gtggacgtaa tgtgatggcc 480
 cttaaagtcg gtgatcgctg tttgatctgc catcactata cttcttacag gtccaagaaa 540
 gcagtccgtg ccttgacaat gccaggattt cattttacag acatccgcct tcagatgctg 600
 aggaaagaga aagacgagta ctttgaactg tacgaagcat ctgtggctag gtacagtgat 660
 cttctgaaa aagcaaattg a 681

<210> 8
 <211> 226
 <212> PRT
 <213> heteractis crispa

<400> 8
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 Thr Val Asn Gly His Tyr Phe Lys Cys Glu Gly Glu Gly Asp Gly Asn
 20 25 30
 Pro Phe Ala Gly Thr Gln Ser Met Arg Ile His Val Thr Glu Gly Ala
 35 40 45
 Pro Leu Pro Phe Ala Phe Asp Ile Leu Ala Pro Cys Cys Glu Tyr Gly
 50 55 60
 Ser Arg Thr Phe Val His His Thr Ala Glu Ile Pro Asp Phe Phe Lys
 65 70 75 80
 Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr Glu
 85 90 95

Asp Gly Gly Ile Leu Thr Ala His Gln Asp Thr Ser Leu Glu Gly Asn
 100 105 110
 Cys Leu Ile Tyr Lys Val Lys Val Leu Gly Thr Asn Phe Pro Ala Asp
 115 120 125
 Gly Pro Val Met Lys Asn Lys Ser Gly Gly Trp Glu Pro Ser Thr Glu
 130 135 140
 Val Val Tyr Pro Glu Asn Gly Val Leu Cys Gly Arg Asn Val Met Ala
 145 150 155 160
 Leu Lys Val Gly Asp Arg Arg Leu Ile Cys His His Tyr Thr Ser Tyr
 165 170 175
 Arg Ser Lys Lys Ala Val Arg Ala Leu Thr Met Pro Gly Phe His Phe
 180 185 190
 Thr Asp Ile Arg Leu Gln Met Leu Arg Lys Glu Lys Asp Glu Tyr Phe
 195 200 205
 Glu Leu Tyr Glu Ala Ser Val Ala Arg Tyr Ser Asp Leu Pro Glu Lys
 210 215 220
 Ala Asn
 225

<210> 9
 <211> 681
 <212> DNA
 <213> heteractis crispa

<400> 9
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 cattattttca agtgtgaagg agagggagac ggcaacccat ttgcaggtag gcagagcatg 120
 aggattcatg tcaccgaagg ggctccatta ccatttgcct tcgacatttt ggcaccgtgt 180
 tgtgcgtacg gcagcaggac ctttgtccac catacggcag agattcccga tttcttcaag 240
 cagtctttcc ctgaaggctt tacttgggaa agaaccacaa cctatgaaga tggaggcatt 300
 cttactgctc atcaggacac aagcctggag gggaactgcc ttatatacaa ggtgaaagtc 360
 cttggtacca attttcctgc tgatggcccc gtgatgaaga acaaatcagg aggatgggag 420
 ccaagcactg aggtggttta tccagagaat ggtgtcctgt gtggacgtaa tgtgatggcc 480
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 gcagtcctg ccttgacaat gccaggattt cattttacag acatccgcct tcagatgctg 600
 agaaaagaga aagacgagta ctttgaactg tacgaagcat ctgtggctag gtacagtgat 660
 cttcctgaaa aagcaaattg a 681

<210> 10
 <211> 226
 <212> PRT
 <213> heteractis crispa

<400> 10
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 20 25 30
 Pro Phe Ala Gly Thr Gln Ser Met Arg Ile His Val Thr Glu Gly Ala
 35 40 45
 Pro Leu Pro Phe Ala Phe Asp Ile Leu Ala Pro Cys Cys Ala Tyr Gly
 50 55 60
 Ser Arg Thr Phe Val His His Thr Ala Glu Ile Pro Asp Phe Phe Lys
 65 70 75 80
 Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr Glu
 85 90 95
 Asp Gly Gly Ile Leu Thr Ala His Gln Asp Thr Ser Leu Glu Gly Asn
 100 105 110
 Cys Leu Ile Tyr Lys Val Lys Val Leu Gly Thr Asn Phe Pro Ala Asp
 115 120 125

Gly Pro Val Met Lys Asn Lys Ser Gly Gly Trp Glu Pro Ser Thr Glu
 130 135 140
 Val Val Tyr Pro Glu Asn Gly Val Leu Cys Gly Arg Asn Val Met Ala
 145 150 155 160
 Leu Lys Val Gly Asp Arg Arg Leu Ile Cys His His Tyr Thr Ser Tyr
 165 170 175
 Arg Ser Lys Lys Ala Val Arg Ala Leu Thr Met Pro Gly Phe His Phe
 180 185 190
 Thr Asp Ile Arg Leu Gln Met Leu Arg Lys Glu Lys Asp Glu Tyr Phe
 195 200 205
 Glu Leu Tyr Glu Ala Ser Val Ala Arg Tyr Ser Asp Leu Pro Glu Lys
 210 215 220
 Ala Asn
 225

<210> 11
 <211> 687
 <212> DNA
 <213> heteractis crispa

<400> 11
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 aacggccact acttcaagtg cgagggcgag ggcgacggca accccttcgc cggcaccag 120
 agcatgagaa tccacgtgac cgagggcgcc cccctgccct tcgcttcga catcctggcc 180
 ccctgctgag agtacggcag caggaccttc gtgcaccaca ccgccgagat cccgacttc 240
 ttcaagcaga gcttccccga gggcttcacc tgggagagaa ccaccaccta cgaggacggc 300
 ggcatacctga ccgcccacca ggacaccagc ctggagggca actgcctgat ctacaagggtg 360
 aaggtgcacg gcaccaactt ccccgccgac ggccccgtga tgaagaacaa gagcggcggc 420
 tgggagccca gcaccgaggt ggtgtacccc gagaacggcg tgctgtgcgg ccggaacgtg 480
 atggccctga aggtggcgga ccggcacctg atctgccacc actacaccag ctaccggagc 540
 aagaaggccg tgcgcgccct gaccatgccc ggcttcact tcaccgacat ccggctccag 600
 atgctgcgga agaagaagga cgagtacttc gagctgtacg aggccagcgt ggcgcgttac 660
 agcgacctgc ccgagaaggc caactga 687

<210> 12
 <211> 227
 <212> PRT
 <213> heteractis crispa

<400> 12
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 Asn Pro Phe Ala Gly Thr Gln Ser Met Arg Ile His Val Thr Glu Gly
 35 40 45
 Ala Pro Leu Pro Phe Ala Phe Asp Ile Leu Ala Pro Cys Cys Glu Tyr
 50 55 60
 Gly Ser Arg Thr Phe Val His His Thr Ala Glu Ile Pro Asp Phe Phe
 65 70 75 80
 Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr
 85 90 95
 Glu Asp Gly Gly Ile Leu Thr Ala His Gln Asp Thr Ser Leu Glu Gly
 100 105 110
 Asn Cys Leu Ile Tyr Lys Val Lys Val His Gly Thr Asn Phe Pro Ala
 115 120 125
 Asp Gly Pro Val Met Lys Asn Lys Ser Gly Gly Trp Glu Pro Ser Thr
 130 135 140
 Glu Val Val Tyr Pro Glu Asn Gly Val Leu Cys Gly Arg Asn Val Met
 145 150 155 160

Ala Leu Lys Val Gly Asp Arg His Leu Ile Cys His His Tyr Thr Ser
165 170 175
Tyr Arg Ser Lys Lys Ala Val Arg Ala Leu Thr Met Pro Gly Phe His
180 185 190
Phe Thr Asp Ile Arg Leu Gln Met Leu Arg Lys Thr Lys Asp Glu Tyr
195 200 205
Phe Glu Leu Tyr Glu Ala Ser Val Ala Arg Tyr Ser Asp Leu Pro Glu
210 215 220
Lys Ala Asn
225

<210> 13
<211> 687
<212> DNA
<213> heteractis crispa

<400> 13
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agcatgcgga tccacgtgac cgagggcgcc cccctgccct tcgccttcga catcctggcc 180
ccctgctgcg agtacggcag caggaccttc gtgcaccaca ccgccgagat ccccgacttc 240
ttcaagcaga gcttccccga gggcttcacc tgggagagaa ccaccaccta cgaggacggc 300
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aaggtgctgg gcaccaactt ccccgccgac ggcccgtga tgaagaacaa gagcggcggc 420
tgggagccca gcaccgaggt ggtgtacccc gagaacggcg tgctgtgctg ccggaacgtg 480
atggccctga aggtgggcca ccggcggtg atctgccacc actacaccag ctaccggagc 540
aagaaggcgc tgcgggccct gaccatgcc ggcttcact tcaccgacat ccgctgcag 600
atgctgcgga aggagaagga cgagtacttc gagctgtacg aggccagcgt ggcccgttac 660
agcgacctgc ccgagaaggc caactga 687

<210> 14
<211> 227
<212> PRT
<213> heteractis crispa

<400> 14
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20 25 30
Asn Pro Phe Ala Gly Thr Gln Ser Met Arg Ile His Val Thr Glu Gly
35 40 45
Ala Pro Leu Pro Phe Ala Phe Asp Ile Leu Ala Pro Cys Cys Glu Tyr
50 55 60
Gly Ser Arg Thr Phe Val His His Thr Ala Glu Ile Pro Asp Phe Phe
65 70 75 80
Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr
85 90 95
Glu Asp Gly Gly Ile Leu Thr Ala His Gln Asp Thr Ser Leu Glu Gly
100 105 110
Asn Cys Leu Ile Tyr Lys Val Lys Val His Gly Thr Asn Phe Pro Ala
115 120 125
Asp Gly Pro Val Met Lys Asn Lys Ser Gly Gly Trp Glu Pro Ser Thr
130 135 140
Glu Val Val Tyr Pro Glu Asn Gly Val Leu Cys Gly Arg Asn Val Met
145 150 155 160
Ala Leu Lys Val Gly Asp Arg Arg Leu Ile Cys His His Tyr Thr Ser
165 170 175
Tyr Arg Ser Lys Lys Ala Val Arg Ala Leu Thr Met Pro Gly Phe His
180 185 190

Phe Thr Asp Ile Arg Leu Gln Met Leu Arg Lys Glu Lys Asp Glu Tyr
 195 200 205
 Phe Glu Leu Tyr Glu Ala Ser Val Ala Arg Tyr Ser Asp Leu Pro Glu
 210 215 220
 Lys Ala Asn
 225

<210> 15
 <211> 1396
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fusion construct

<400> 15
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 cgccggcacc cagagcatgc ggatccacgt gaccgagggc gccccctgc ctttcgcctt 180
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 cagctaccgg agcaagaagg ccgtgcgggc cctgaccatg cccggcttcc acttcaccga 600
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 cttcaagtgc gagggcgagg gcgacggcaa ccccttcgcc ggcaccaga gcatgcggat 840
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 gtacggcagc aggaccttcg tgcaccacac cgccgagatc cccgacttct tcaagcagag 960
 cttccccgag ggcttcacct gggagagaa caccacctac gaggaaggcg gcatcctgac 1020
 cgcccaccag gacaccagcc tggagggcaa ctgcctgac tacaaggtga aggtgctggg 1080
 caccaacttc cccgcccagc gccccgtgat gaagaacaag agcggcggct gggagcccag 1140
 caccgaggtg gtgtacccc agaacggcgt gctgtgcggc cggaacgtga tggccctgaa 1200
 ggtgggcgac cggcggctga tctgccacca ctacaccagc taccggagca agaaggccgt 1260
 gcgggccctg accatgcccg gcttccactt caccgacatc cggctgcaga tgctgcggaa 1320
 ggagaaggac gagtacttcg agctgtacga ggccagcgtg gcccggtaca gcgacctgcc 1380
 cgagaaggcc aactga 1396

<210> 16
 <211> 460
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion construct

<400> 16
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 Glu Gly Thr Val Asn Gly His Tyr Phe Lys Cys Glu Gly Glu Gly Asp
 20 25 30
 Gly Asn Pro Phe Ala Gly Thr Gln Ser Met Arg Ile His Val Thr Glu
 35 40 45
 Gly Ala Pro Leu Pro Phe Ala Phe Asp Ile Leu Ala Pro Cys Cys Glu
 50 55 60
 Tyr Gly Ser Arg Thr Phe Val His His Thr Ala Glu Ile Pro Asp Phe
 65 70 75 80

Phe	Lys	Gln	Ser	Phe	Pro	Glu	Gly	Phe	Thr	Trp	Glu	Arg	Thr	Thr	Thr
				85					90					95	
Tyr	Glu	Asp	Gly	Gly	Ile	Leu	Thr	Ala	His	Gln	Asp	Thr	Ser	Leu	Glu
			100					105					110		
Gly	Asn	Cys	Leu	Ile	Tyr	Lys	Val	Lys	Val	Leu	Gly	Thr	Asn	Phe	Pro
		115					120					125			
Ala	Asp	Gly	Pro	Val	Met	Lys	Asn	Lys	Ser	Gly	Gly	Trp	Glu	Pro	Ser
	130					135					140				
Thr	Glu	Val	Val	Tyr	Pro	Glu	Asn	Gly	Val	Leu	Cys	Gly	Arg	Asn	Val
145					150					155					160
Met	Ala	Leu	Lys	Val	Gly	Asp	Arg	Arg	Leu	Ile	Cys	His	His	Tyr	Thr
				165					170					175	
Ser	Tyr	Arg	Ser	Lys	Lys	Ala	Val	Arg	Ala	Leu	Thr	Met	Pro	Gly	Phe
			180					185					190		
His	Phe	Thr	Asp	Ile	Arg	Leu	Gln	Met	Leu	Arg	Lys	Glu	Lys	Asp	Glu
	195					200						205			
Tyr	Phe	Glu	Leu	Tyr	Glu	Ala	Ser	Val	Ala	Arg	Tyr	Ser	Asp	Leu	Pro
	210					215					220				
Glu	Lys	Ala	Asn	Arg	Ser	Pro	Gly	Met	Val	Ser	Gly	Leu	Leu	Lys	Glu
225					230					235				240	
Ser	Met	Arg	Ile	Lys	Met	Tyr	Met	Glu	Gly	Thr	Val	Asn	Gly	His	Tyr
				245					250					255	
Phe	Lys	Cys	Glu	Gly	Glu	Gly	Asp	Gly	Asn	Pro	Phe	Ala	Gly	Thr	Gln
			260					265					270		
Ser	Met	Arg	Ile	His	Val	Thr	Glu	Gly	Ala	Pro	Leu	Pro	Phe	Ala	Phe
		275					280					285			
Asp	Ile	Leu	Ala	Pro	Cys	Cys	Glu	Tyr	Gly	Ser	Arg	Thr	Phe	Val	His
	290					295					300				
His	Thr	Ala	Glu	Ile	Pro	Asp	Phe	Phe	Lys	Gln	Ser	Phe	Pro	Glu	Gly
305					310					315				320	
Phe	Thr	Trp	Glu	Arg	Thr	Thr	Thr	Tyr	Glu	Asp	Gly	Gly	Ile	Leu	Thr
				325					330					335	
Ala	His	Gln	Asp	Thr	Ser	Leu	Glu	Gly	Asn	Cys	Leu	Ile	Tyr	Lys	Val
			340					345					350		
Lys	Val	Leu	Gly	Thr	Asn	Phe	Pro	Ala	Asp	Gly	Pro	Val	Met	Lys	Asn
	355						360					365			
Lys	Ser	Gly	Gly	Trp	Glu	Pro	Ser	Thr	Glu	Val	Val	Tyr	Pro	Glu	Asn
	370					375					380				
Gly	Val	Leu	Cys	Gly	Arg	Asn	Val	Met	Ala	Leu	Lys	Val	Gly	Asp	Arg
385					390					395				400	
Arg	Leu	Ile	Cys	His	His	Tyr	Thr	Ser	Tyr	Arg	Ser	Lys	Lys	Ala	Val
				405					410					415	
Arg	Ala	Leu	Thr	Met	Pro	Gly	Phe	His	Phe	Thr	Asp	Ile	Arg	Leu	Gln
			420					425					430		
Met	Leu	Arg	Lys	Glu	Lys	Asp	Glu	Tyr	Phe	Glu	Leu	Tyr	Glu	Ala	Ser
	435					440						445			
Val	Ala	Arg	Tyr	Ser	Asp	Leu	Pro	Glu	Lys	Ala	Asn				
	450					455					460				

<210> 17
 <211> 1424
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fusion construct

<400> 17
 accggtcgcc accatggtga gcggcctgct gaaggagagc atgcgcatca agatgtacat 60
 ggagggcacc gtgaacggcc actacttcaa gtgcgagggc gagggcgacg gcaaccctt 120

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cgccggcacc cagagcatgc ggatccacgt gaccgagggc gccccctgc ccttcgcctt 180
cgacatcctg gccccctgct gcgagtagcg cagcaggacc ttctgtgcacc acaccgccga 240
gatccccgac ttcttcaagc agagcttccc cgagggtctc acctgggaga gaaccaccac 300
ctacgaggac ggcggcacatc tgaccgcca ccaggacacc agcctggagg gcaactgcct 360
gatctacaag gtgaaggtgc tgggcaccaa cttccccgcc gacggccccg tgatgaagaa 420
caagagcggc ggctgggagc ccagcaccga ggtggtgtac cccgagaacg gcgtgctgtg 480
cggccggaac gtgatggccc tgaaggtggg cgaccggcgg ctgatctgcc accactacac 540
cagctaccgg agcaagaagg ccgtgcgggc cctgaccatg cccggcttcc acttcaccga 600
catccggctg cagatgctgc ggaaggagaa ggacgagtag ttcgagctgt acgaggccag 660
cgtggccccg tacagcgacc tgcccagaaa ggccaacaga tctccccgga tggtagcg 720
cctgctgaag gagagcatgc gcatcaagat gtacatggag ggcaccgtga acggccacta 780
cttcaagtgc gaggcgaggg gcgacggcaa ccccttcgcc ggcaccaga gcatgcggat 840
ccacgtgacc gaggcgcccc ccctgccctt cgccttcgac atcctggccc cctgctgcga 900
gtacggcagc aggaccttcg tgcaaccac cgccgagatc cccgacttct tcaagcagag 960
cttccccgag ggcttcacct gggagagaac caccacctac gaggacggcg gcatcctgac 1020
cgccaccag gacaccagcc tggagggcaa ctgacctgat tacaaggtga aggtgctggg 1080
caccaacttc cccgcccagc gcccgctgat gaagaacaag agcggcggct gggagcccag 1140
caccgaggtg gtgtaccccc agaacggcgt gctgtgcggc cggaacgtga tggccctgaa 1200
ggtgggcgac cggcggtga tctgccacca ctacaccagc tacggagca agaaggcgt 1260
gcgggcccct accatgccc gctccactt caccgacatc cggctgcaga tgctgcggaa 1320
ggagaaggac gactacttcg agctgtacga ggccagcgtg gcccggtaca gcgacctgcc 1380
cgagaaggcc aacagaactc gagctatgga tgatgatatc gccg 1424

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<210> 18
 <211> 470
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion construct

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<400> 18
Met Val Ser Gly Leu Leu Lys Glu Ser Met Arg Ile Lys Met Tyr Met
  1           5           10           15
Glu Gly Thr Val Asn Gly His Tyr Phe Lys Cys Glu Gly Glu Gly Asp
           20           25           30
Gly Asn Pro Phe Ala Gly Thr Gln Ser Met Arg Ile His Val Thr Glu
           35           40           45
Gly Ala Pro Leu Pro Phe Ala Phe Asp Ile Leu Ala Pro Cys Cys Glu
           50           55           60
Tyr Gly Ser Arg Thr Phe Val His His Thr Ala Glu Ile Pro Asp Phe
           65           70           75           80
Phe Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr
           85           90           95
Tyr Glu Asp Gly Gly Ile Leu Thr Ala His Gln Asp Thr Ser Leu Glu
           100          105          110
Gly Asn Cys Leu Ile Tyr Lys Val Lys Val Leu Gly Thr Asn Phe Pro
           115          120          125
Ala Asp Gly Pro Val Met Lys Asn Lys Ser Gly Gly Trp Glu Pro Ser
           130          135          140
Thr Glu Val Val Tyr Pro Glu Asn Gly Val Leu Cys Gly Arg Asn Val
           145          150          155          160
Met Ala Leu Lys Val Gly Asp Arg Arg Leu Ile Cys His His Tyr Thr
           165          170          175
Ser Tyr Arg Ser Lys Lys Ala Val Arg Ala Leu Thr Met Pro Gly Phe
           180          185          190
His Phe Thr Asp Ile Arg Leu Gln Met Leu Arg Lys Glu Lys Asp Glu
           195          200          205
Tyr Phe Glu Leu Tyr Glu Ala Ser Val Ala Arg Tyr Ser Asp Leu Pro
           210          215          220
Glu Lys Ala Asn Arg Ser Pro Gly Met Val Ser Gly Leu Leu Lys Glu

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225		230		235		240
Ser Met Arg Ile Lys	Met Tyr Met Glu Gly	Thr Val Asn Gly	His Tyr			
	245	250	255			
Phe Lys Cys Glu Gly	Glu Gly Asp Gly	Asn Pro Phe Ala	Gly Thr Gln			
	260	265	270			
Ser Met Arg Ile His	Val Thr Glu Gly	Ala Pro Leu Pro	Phe Ala Phe			
	275	280	285			
Asp Ile Leu Ala Pro	Cys Cys Glu Tyr Gly	Ser Arg Thr Phe	Val His			
	290	295	300			
His Thr Ala Glu Ile	Pro Asp Phe Phe Lys	Gln Ser Phe Pro	Glu Gly			
305	310	315	320			
Phe Thr Trp Glu Arg	Thr Thr Thr Tyr Glu	Asp Gly Gly Ile	Leu Thr			
	325	330	335			
Ala His Gln Asp Thr	Ser Leu Glu Gly	Asn Cys Leu Ile	Tyr Lys Val			
	340	345	350			
Lys Val Leu Gly Thr	Asn Phe Pro Ala	Asp Gly Pro Val	Met Lys Asn			
	355	360	365			
Lys Ser Gly Gly Trp	Glu Pro Ser Thr Glu	Val Val Tyr Pro	Glu Asn			
	370	375	380			
Gly Val Leu Cys Gly	Arg Asn Val Met Ala	Leu Lys Val Gly	Asp Arg			
385	390	395	400			
Arg Leu Ile Cys His	His Tyr Thr Ser Tyr	Arg Ser Lys Lys	Ala Val			
	405	410	415			
Arg Ala Leu Thr Met	Pro Gly Phe His Phe	Thr Asp Ile Arg	Leu Gln			
	420	425	430			
Met Leu Arg Lys Glu	Lys Asp Glu Tyr Phe	Glu Leu Tyr Glu	Ala Ser			
	435	440	445			
Val Ala Arg Tyr Ser	Asp Leu Pro Glu Lys	Ala Asn Arg Thr	Arg Ala			
	450	455	460			
Met Asp Asp Asp Ile	Ala					
465	470					

<210> 19
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 19
 acatggatcc gctggtttgt tgaaaga

27

<210> 20
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 20
 acctcagtgc ttggtccca t

21

<210> 21
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>

<223> primer

<400> 21

atgggagcca agcactgagg t

21

<210> 22

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 22

tgacaagctt ctggtgtcac tgggaacaat ca

32

<210> 23

<211> 684

<212> DNA

<213> heteractis crispa

<400> 23

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ggccattatt tcaagtgtga aggagagggga gacggcaacc catttacagg tacgcagagc 120
atgaggattc atgtcaccga agggggtcca ttaccatttg ccttcgacat tttggcaccg 180
tgttgtgagt acggcagcag gacctttgtc caccatacgg cagagattcc cgatttcttc 240
aagcagtctt tccctgaagg ctttacttgg gaaagaacca caacctatga agatggaggc 300
attcttactg ctcacacagga cacaagcctg gaggggaact gccttatata caaggtgaaa 360
gtccttggtg ccaattttcc tgctgatggc cccgtgatga agaacaaatc aggaggatgg 420
gagccaagca ctgaggtggt ttatccagag aatggtgtcc tgtgtggacg taatgtgatg 480
gcccttaaag tcggtgatcg tcgtttgatc tgccatctct atactttctta caggtccaag 540
aaagcagtcc gtgccttgac aatgccagga tttcatttta cagacatccg cttcagatg 600
ccgagggaaa agaaagacga gtactttgaa ctgtacgaag catctgtggc taggtacagt 660
gatcttctcg aaaaagcaaa ttga 684

<210> 24

<211> 227

<212> PRT

<213> heteractis crispa

<400> 24

Met	Ala	Gly	Leu	Leu	Lys	Glu	Ser	Met	Arg	Ile	Lys	Met	Tyr	Met	Glu
1			5						10				15		
Gly	Thr	Val	Asn	Gly	His	Tyr	Phe	Lys	Cys	Glu	Gly	Glu	Gly	Asp	Gly
			20					25					30		
Asn	Pro	Phe	Thr	Gly	Thr	Gln	Ser	Met	Arg	Ile	His	Val	Thr	Glu	Gly
		35					40					45			
Ala	Pro	Leu	Pro	Phe	Ala	Phe	Asp	Ile	Leu	Ala	Pro	Cys	Cys	Glu	Tyr
	50					55					60				
Gly	Ser	Arg	Thr	Phe	Val	His	His	Thr	Ala	Glu	Ile	Pro	Asp	Phe	Phe
65					70					75				80	
Lys	Gln	Ser	Phe	Pro	Glu	Gly	Phe	Thr	Trp	Glu	Arg	Thr	Thr	Thr	Tyr
				85					90					95	
Glu	Asp	Gly	Gly	Ile	Leu	Thr	Ala	His	Gln	Asp	Thr	Ser	Leu	Glu	Gly
			100					105					110		
Asn	Cys	Leu	Ile	Tyr	Lys	Val	Lys	Val	Leu	Gly	Thr	Asn	Phe	Pro	Ala
		115					120					125			
Asp	Gly	Pro	Val	Met	Lys	Asn	Lys	Ser	Gly	Gly	Trp	Glu	Pro	Ser	Thr
	130					135					140				
Glu	Val	Val	Tyr	Pro	Glu	Asn	Gly	Val	Leu	Cys	Gly	Arg	Asn	Val	Met
145					150					155					160

Ala Leu Lys Val Gly Asp Arg Arg Leu Ile Cys His Leu Tyr Thr Ser
 165 170 175
 Tyr Arg Ser Lys Lys Ala Val Arg Ala Leu Thr Met Pro Gly Phe His
 180 185 190
 Phe Thr Asp Ile Arg Leu Gln Met Pro Arg Lys Lys Lys Asp Glu Tyr
 195 200 205
 Phe Glu Leu Tyr Glu Ala Ser Val Ala Arg Tyr Ser Asp Leu Pro Glu
 210 215 220
 Lys Ala Asn
 225

<210> 25
 <211> 680
 <212> DNA
 <213> heteractis crispa

<400> 25
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 cattatttca agtgtgaagg agagggagac ggcaacccat ttgcaggtag gcagagcatg 120
 aggattcatg tcaccgaagg ggctccatta ccatttgcct tcgacatttt ggcaccgtgt 180
 tgtgcgtacg gcagcaggac ctttgtccac catacggcag agattcccga tttcttcaag 240
 cagtctttcc ctgaaggctt tacttgggaa agaaccacaa cctatgaaga tggaggcatt 300
 cttactgctc atcaggacac aagcctggag gggaaactgcc ttatatacaa ggtgaaagtc 360
 cttggtacca attttctgct tgatggcccc gtgatgaaga aaaatcagga ggatgggagc 420
 caagcactga ggtggtttat ccagagaatg gtgtcctgtg tggacgtaat gtgatggccc 480
 ttaaagtcgg tgatcgtcgt ttgatctgcc atcactatac ttcttacagg tccaagaaag 540
 cagtccgtgc cttgacaatg ccaggatttc attttacaga catccgcctt cagatgctga 600
 ggaaaaagaa agacgagtag tttgaactgt acgaagcatc tgtggctagg tacagtgate 660
 ttcttgaaaa agcaaattga 680

<210> 26
 <211> 226
 <212> PRT
 <213> heteractis crispa

<400> 26
 Ser Gly Leu Leu Lys Glu Ser Met Arg Ile Lys Met Tyr Met Glu Gly
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 Thr Val Asn Gly His Tyr Phe Lys Cys Glu Gly Glu Gly Asp Gly Asn
 20 25 30
 Pro Phe Ala Gly Thr Gln Ser Met Arg Ile His Val Thr Glu Gly Ala
 35 40 45
 Pro Leu Pro Phe Ala Phe Asp Ile Leu Ala Pro Cys Cys Ala Tyr Gly
 50 55 60
 Ser Arg Thr Phe Val His His Thr Ala Glu Ile Pro Asp Phe Phe Lys
 65 70 75 80
 Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr Glu
 85 90 95
 Asp Gly Gly Ile Leu Thr Ala His Gln Asp Thr Ser Leu Glu Gly Asn
 100 105 110
 Cys Leu Ile Tyr Lys Val Lys Val Leu Gly Thr Asn Phe Pro Ala Asp
 115 120 125
 Gly Pro Val Met Lys Asn Lys Ser Gly Gly Trp Glu Pro Ser Thr Glu
 130 135 140
 Val Val Tyr Pro Glu Asn Gly Val Leu Cys Gly Arg Asn Val Met Ala
 145 150 155 160
 Leu Lys Val Gly Asp Arg Arg Leu Ile Cys His His Tyr Thr Ser Tyr
 165 170 175
 Arg Ser Lys Lys Ala Val Arg Ala Leu Thr Met Pro Gly Phe His Phe
 180 185 190

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Thr Asp Ile Arg Leu Gln Met Leu Arg Lys Lys Lys Asp Glu Tyr Phe
 195 200 205
 Glu Leu Tyr Glu Ala Ser Val Ala Arg Tyr Ser Asp Leu Pro Glu Lys
 210 215 220
 Ala Asn
 225

<210> 27
 <211> 910
 <212> DNA
 <213> heteractis crispa

<400> 27
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 tcttctcctt ggatccttac catggctggt ttgttgaaag aaagtatgcg catcaagatg 120
 tacatggaag gcacggttaa tggccattat ttcaagtgtg aaggagaggg agacggcaac 180
 ccatttacag gtacgcagag catgaggatt catgtcaccg aaggggctcc attaccattt 240
 gccttcgaca ttttggcacc gtgttgtag tacggcagca ggacctttgt ccaccatacg 300
 gcagagattc ccgatttctt caagcagtct ttcctgaag gctttacttg ggaaagaacc 360
 acaacctatg aagatggagg cattcttact gtcctcagg acacaagcct ggaggggaac 420
 tgccttatat acaaggtgaa agtccttggt accaattttc ctgctgatgg ccccgatg 480
 aagaacaaat caggaggatg ggagccatgc actgaggtgg tttatccaga gaatggtgtc 540
 ctgtgtggac gtaatgtgat ggcccttaaa gtcggtgatc gtcgtttgat ctgccatctc 600
 tatacttctt acaggtccaa gaaagcagtc cgtgccttga caatgccagg atttcatttt 660
 acagacatcc gccttcagat gccgaggaaa acgaaagacg agtactttga actgtacgaa 720
 gcatctgtgg ctaggtagag tgatcttcct gaaaaagcaa attgattggt cccagtgcac 780
 ccagactgct gtcagctttt gggttaaagcc cgaaagacaa aaggacattt gtagtttagt 840
 ttatatttcc ctttcatttg tgaatcaaca ttgtactctc tgtaaaccct taaaatgctc 900
 cattaacac 910

<210> 28
 <211> 227
 <212> PRT
 <213> heteractis crispa

<400> 28
 Met Ala Gly Leu Leu Lys Glu Ser Met Arg Ile Lys Met Tyr Met Glu
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 Gly Thr Val Asn Gly His Tyr Phe Lys Cys Glu Gly Glu Gly Asp Gly
 20 25 30
 Asn Pro Phe Thr Gly Thr Gln Ser Met Arg Ile His Val Thr Glu Gly
 35 40 45
 Ala Pro Leu Pro Phe Ala Phe Asp Ile Leu Ala Pro Cys Cys Glu Tyr
 50 55 60
 Gly Ser Arg Thr Phe Val His His Thr Ala Glu Ile Pro Asp Phe Phe
 65 70 75 80
 Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr
 85 90 95
 Glu Asp Gly Gly Ile Leu Thr Ala His Gln Asp Thr Ser Leu Glu Gly
 100 105 110
 Asn Cys Leu Ile Tyr Lys Val Lys Val Leu Gly Thr Asn Phe Pro Ala
 115 120 125
 Asp Gly Pro Val Met Lys Asn Lys Ser Gly Gly Trp Glu Pro Cys Thr
 130 135 140
 Glu Val Val Tyr Pro Glu Asn Gly Val Leu Cys Gly Arg Asn Val Met
 145 150 155 160
 Ala Leu Lys Val Gly Asp Arg Arg Leu Ile Cys His Leu Tyr Thr Ser
 165 170 175
 Tyr Arg Ser Lys Lys Ala Val Arg Ala Leu Thr Met Pro Gly Phe His
 180 185 190

Phe	Thr	Asp	Ile	Arg	Leu	Gln	Met	Pro	Arg	Lys	Thr	Lys	Asp	Glu	Tyr
		195					200					205			
Phe	Glu	Leu	Tyr	Glu	Ala	Ser	Val	Ala	Arg	Tyr	Ser	Asp	Leu	Pro	Glu
	210					215					220				
Lys	Ala	Asn													
225															

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